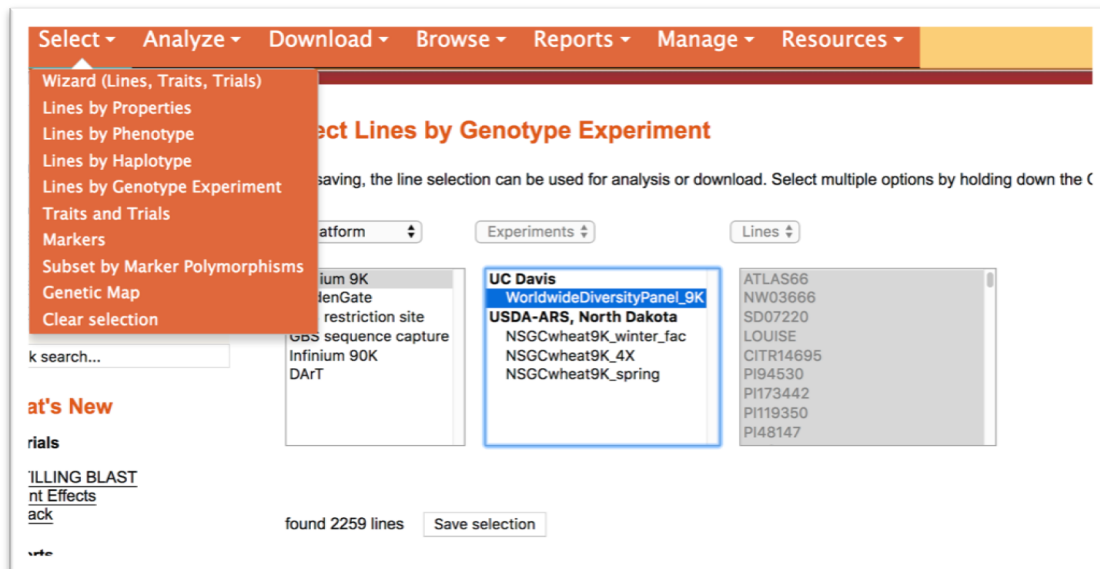


TASSEL is a Java platform for analysis of crop genomic diversity. It provides functionality for association studies, linkage, principal component analysis, cluster analysis, imputation and data visualization. The software is provided by the [Buckler Lab for Maize Genetics and Diversity](#). The program is available from [TASSEL Download](#). Data from T3 website can be accessed by saving from T3 then importing into TASSEL.

Requirements: TASSEL works with several file formats. The preferred format is VCF because the data from T3 is sorted by position as required by TASSEL. If you use the Hapmap format you may have to sort the data using the tool provided in TASSEL. The “pos” column has to be an integer so values from a genetic map are multiplied by 1000 then converted to integer. If a marker location is not defined in the map then that marker is removed. If two markers are defined at the same location then the duplicate ones are removed.

Download data from T3 website then import the data into TASSEL

1. The data can be selected by Select => Wizard or Select => Lines by Genotype Experiment



2. Go to Select => Genetic Map

Map Sets

This table lists the total markers in each map. If a marker is not in the the selected map set then it will be assigned to ch

select	markers (total)	markers (in selected lines)	map set name	comment (select item for complete te
<input type="radio"/>	877		Aegilops tauschii, 2009	From Luo et al, (2009) PNAS 106(37
<input type="radio"/>	19720		SynOp GBS BinMap, 2012	Bin map of Synthetic W9784 x Opata bet
<input type="radio"/>	1485		SynOp GBS AntMap, 2012	Genetic linkage map of Synthetic W9
<input type="radio"/>	1625		KleinProteo x KleinChaja, 2012	Contacts: Jorge Dubcovsky, Luxmi Tr
<input type="radio"/>	3503		w SNP 2013 Consensus	Consensus w SNP map from C.R. Cav
<input type="radio"/>	38832		90K Array Consensus	From: Wang et. al. (2014) Characteri
<input type="radio"/>	125340		CSS POPSEQ 2014	A genetic map created by locating the
<input type="radio"/>	3393777		CSS GBS 2014	A physical map of GBS markers start a
<input checked="" type="radio"/>	168455		RefSeq v1.0	A physical map from IWGSC RefSeq
<input type="radio"/>	145004		Chromosome Survey Sequence, 2014	A physical map from the Chromosom Genome

3. Go to Download => Genotype and Phenotype Data - Select VCF format
4. Select "Create File"

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Resources ▾

Genotype and Phenotype Data
SNP Alleles and Sequences
Marker Annotation
Bulk Download
Android Field Book
Weather Data
Genetic Maps

Genotype and Phenotype Data

to retrieve the results.

consensus ☒ Genotype single experiment

Lines	Markers	Traits	Trials
ATLAS66 NW03666 SD07220 LOUISE CITR14695 PI94530 PI173442 PI119350 PI48147	All	none selected	none selected

Minimum MAF \geq 5 % Remove markers missing > 50 % of data

Removed by filtering	Remaining
73 markers have a minor allele frequency (MAF) less than 5% 0 markers are missing more than 50% of data 73 markers removed	6232 markers

Create file

SNP data coded as {A,C,T,G,N,+,-}
tab delimited
used by **TASSEL**

file type "Hapmap"
for genetic maps the value in pos column is multiplied by 1000 and cor

Create file

genotype coded as {AA=1, BB=-1, AB=0, missing=NA}
comma delimited
used by **rrBLUP**

read.table("snpfile.txt", header=TRUE, check.names=FALSE)
read.table("genotyp.hmp.txt", header=TRUE, check.names=FALSE)

Create file

genotype coded as {AA, AB, BB}
used by **Flapjack**

Create file

VCF format
used by **TASSEL**

Create file

VCF format
Impute missing genotypes using Beagle

using beagle.10Jun18.811.jar (version 5.0)

5. In TASSEL select File => Open then select genotype.vcf file.

